

Figure 1

The initial three residues MVD have been introduced due to restriction sites

P26A		0.38	1.02	-0.07	0.39	0.55	0.85	-0.06	0.4	0.85
	MVDFLRGRAYGL - PYLFWLAAL - HRCQAIRKK - RRIYDLIEL - VQPPQLTLQV-GLCTLVAML - RLRAEAQVK - IEDPPFNSL - YLLEMLWRL-	0.18	0.43	0.83	0.2	0.45	0.83	0.32	0.47	0.83
	GQGGSPTAM - AVLLHEESM - IALYLQQNWWTL-RAKFKQIL - SSCSSCPLSKI- TYGPVFMCL-QAKWRLQTL- RPPIFIRRL- VSFIEFGW-	0.34	0.52	0.82	0.35	0.53	0.71	0.36		
	YPLHEQHGM - VEITPYKPTW- CLGGLTMV - EENLLDFVR - TYSAGINQI - LLDVRFMGV - EGGVGWRHW - HHHHHH (SEQ ID NO:94)									
P26B		0.38	1.02	-0.07	0.39	0.85	-0.06	0.4	0.53	0.71
	MVDFLRGRAYGL - PYLFWLAAL - HRCQAIRKK - RRIYDLIEL- GLCTLVAML- RLRAEAQVK- IEDPPFNSL -TYSAGINQI- LLDVRFMGV-	0.36	0.83	0.2	0.45	0.83	0.32	0.47	0.83	0.34
	EGGVGWRHW - IALYLQQNWWTL - RAKFKQIL - SSCSSCPLSKI - TYGPVFMCL - QAKWRLQTL - RPPIFIRRL - VSFIEFGW - YPLHEQHGM-	0.52	0.82	0.35	0.85	0.18	0.43	0.55		
	VEITPYKPTW - CLGGLTMV - EENLLDFVR - YLLEMLWRL - GQGGSP TAM - AVLLEESM -VQPPQLTLQV -HHHHHH (SEQ ID NO:95)									

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Hydrophobicity Index (Fauschere & Pliska)

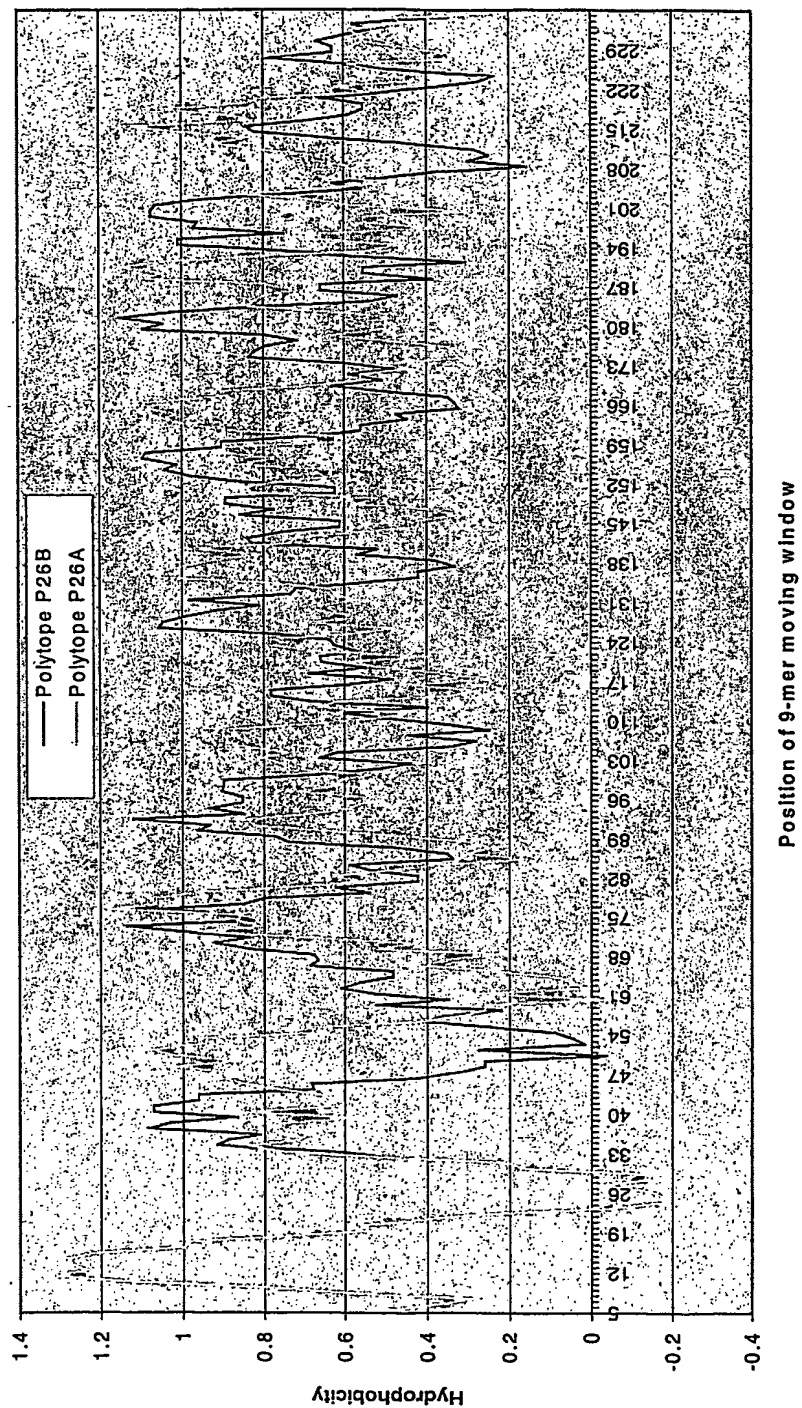


Figure 2

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Figure 3A gp350/PT26A

MEDPGFFNVEIPEFPFYPTCNVCTADVNTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENAT
 T-help epitope 70
 NLFLLELLGAGELALTMRSKKLPIINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPY
 140
 IKWDNDCNSTNITAVVRAQGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPDGNKFN
 T-help epitope 210
 ITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCI
 280
 QSNIVFSDEIPASQDMPTNTTDDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLT
 350
 SGTSPGCENISGAFASNRTFDITVSGLGTA PKTLIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGF
 420
 ADPNTTTGVDFLRGRAYGLPYLFWLA⁴²⁸AIHRCQAIRKKRRIYDLIELVQPPQ^{B8}LT^{A23}LQVGLCTLVAMLR^{B27}RLRAE^{B27}
^{B46}
 AOVKIEDPPFNSLYLLEMLWRLGQGSPTAMAVLLHEESMIALYLOQNW^{A2}WTLRAKFKQLLSSC^{A3}SSCPLSK
^{B60} ^{A2} ^{B62} ^{B35} ^{B57/A2} ^{B8} ^{A11}
 ITYGPVFMCLQAKWRLQTLRPPIFIRRLVSFIEFVGWYPLHEQHGMVEITPYKPTWCLGGLLT^{A24}MTVEENLL^{B8}
 DFVRFTYSAGIVQILLDFVRFMGVEGGVGWRHWHHHHHH^{B7}
 B44 ^{A24} ^{A2} ^{B44 (SEQ ID NO:96)}

Figure 3B gp350/PT26B

MEDPGFFNVEIPEFPFYPTCNVCTADVNTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENAT
 T-help epitope 70
 NLFLLELLGAGELALTMRSKKLPIINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPY
 140
 IKWDNDCNSTNITAVVRAQGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPDGNKFN
 T-help epitope 210
 ITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCI
 280
 QSNIVFSDEIPASQDMPTNTTDDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLT
 350
 SGTSPGCENISGAFASNRTFDITVSGLGTA PKTLIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGF
 420
 ADPNTTTGVDFLRGRAYGLPYLFWLA⁴²⁸AIHRCQAIRKKRRIYDLIELGLCTLVAMLR^{B8}RLRAEAQ VKIEDPPF^{A23}
^{B27} ^{B27} ^{A2} ^{A3} ^{B60}
 NSLTYSAGIVQILLDFVRFMGVEGGVGWRHWIALYLOQNW^{A24}WTLRAKFKQLLSSC^{A2}SSCPLSKITYGPV^{A11}FMCA^{A24}
^{B8} ^{B7} ^{B58} ^{B35} ^{B44} ^{A2} ^{B44}
 LQAKWRLQTLRPPIFIRRLVSFIEFVGWYPLHEQHGMVEITPYKPTWCLGGLLTMTVEENLLDFVRFYLL
 MLWRLGQGSPTAMAVLLHEESMVQPPQ^{A2}LT^{B62}LQVHHHHHHH (SEQ ID NO:97)
^{B35} ^{B46}

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Figure 4A

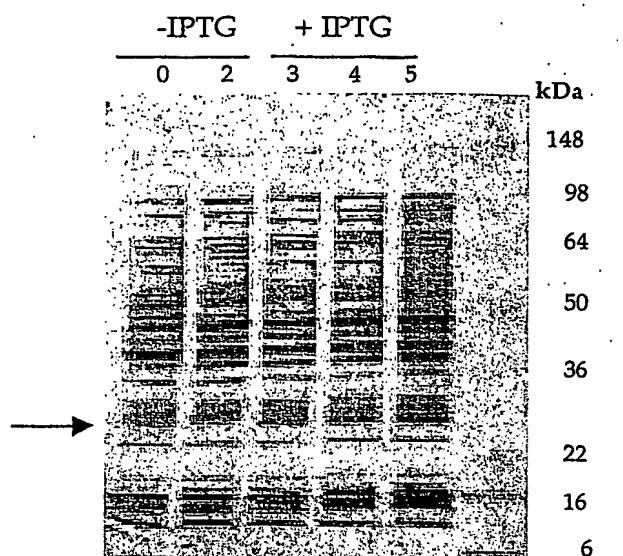


Figure 4B

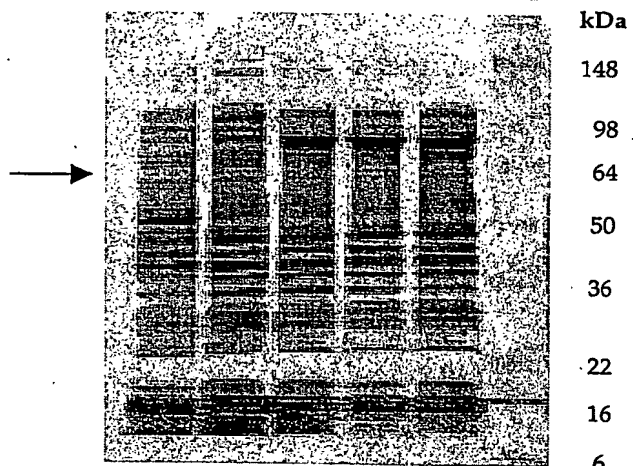


Figure 4C

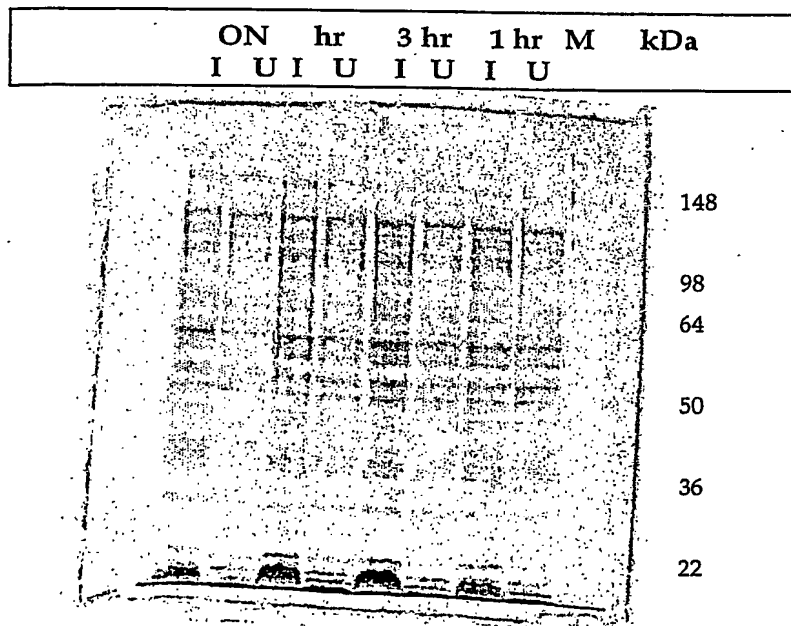


Figure 5

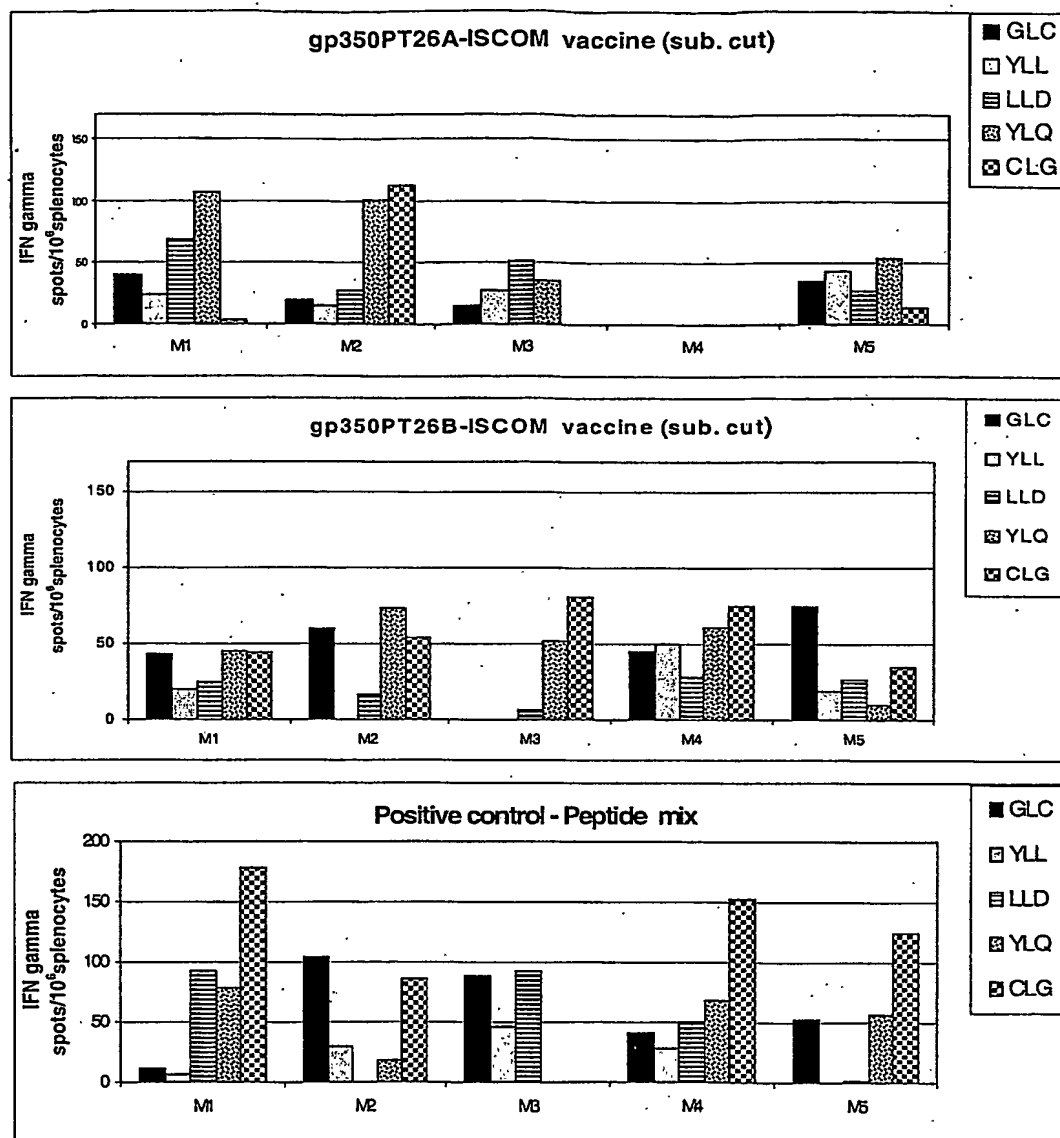


Figure 6

EBV-NPc _a	1.02	-0.07	0.82	0.98	-0.06	0.4	0.88	0.01	0.45	0.85
SSCSCPLSKI - HRCQAIRKK - CLGGLTMTV - LTAGFLIFL - RLRAEAQVK - IEDPPFNSL - LLSAWILTA - RRRWRRLTV - PYLFWLAAI - YLLEMLWRL -	0.18	0.64	0.85	0.20	0.67	0.83	0.32	0.71	0.34	0.78
GQGGSP TAM - VMSNTLLSAW - ALLVLYSFA - RAKFKQLL - IALYLOQNW - TYGPFVMCL - QAKWRLOTL - YLQONWWTL - YPLHEQHGM - CPLSKILL -	0.04									
HHHHHH (SEQ ID NO:98)										

HIVa																
0.98	-0.26	0.44	0.8	-0.16	0.44	0.76	-0.02	0.45	0.71							
IPVAVALV - RLRPGGKK - ILKEPVHG - PLVKLWYQL - RPKGKKYKL - KYKLKHIVW - TWETWWTEYW - EIKDTKEAL - KRWILGLNK - KLWVTVVYGV -																
0.14	0.47	0.69	0.22	0.48	0.69	0.27	0.5	0.67	0.35	0.53						
KIEELRQHL - MTNNPPV - VTLWQRPLV - WASRELERF - LLWKGEVAV - YTAFTPSI - IYQEPFKNLK - SLYNTVATL - AIRILQQL - AIFQSSMTK - VIYQYMDDL -																
0.61	0.36	0.57	0.59	0.57	0.04											
LVGPTPVNI - TPQDLNTML - YLAWVPAHK - ALVEICTEM - TLNAWVKV - HHHHHH (SEQ ID NO:99)																
HI values (n=3): 1.16 0.98 1.08 1.04 1.18 1.19 1.14 1.30 1.32 1.30 1.38 1.39 1.44 1.46 1.52 1.55 1.49 1.50 1.54 1.52 1.73 1.20																
HIVb																
0.44	0.45	0.57	0.14	0.69	0.22	0.8	0.61	0.98	0.5	0.47						
ILKEPVHG - KRWILGLNK - TLNAWVKV - KIEELRQHL - YTAFTPSI - WASRELERF - PLVKLWYQL - LVGPTPVNI - IPVAVALV - SLYNTVATL - MTNNPPV -																
0.48	0.76	0.35	-0.26	0.59	0.71	0.57	0.67	-0.02	0.69							
LLWKGEVAV - TWETWWTEYW - AIFQSSMTK - RLRPGGKK - ALVEICTEM - KLWVTVVYGV - YLAWVPAHK - AIRILQQL - EIKDTKEAL - VTLWQRPLV -																
0.27	0.53	0.36	-0.16	0.44	0.04											
IYQEPFKNLK - VIYQYMDDL - TPQDLNTML - RPKGKKYKL - KYKLKHIVW - HHHHHH (SEQ ID NO:100)																
HI values (n=3): 1.46 1.16 1.40 1.05 1.71 1.63 2.39 2.09 1.95 1.45 1.71 1.59 0.85 0.68 1.04 1.87 1.95 1.22 1.34 0.94 1.49 1/16 0.73 0.64 0.32																

	0.94	-0.3	0.61	0.9	-0.07	0.47	0.82	0.15	0.51	0.75
LLFNILGGWV - KTSERSQPR - FULLADARV - LLFLLLLADA - RLGVRATRK - GVAGALVAFK - LPGCSFSIF - RMYVGGVEHR - VAGALVAFK - DLMGYPLV -										
LIFCHSKKK - ILACYGAGV - HMWNFISGI - QLFTFSPRR - VGIYLLPNR - FWAKHMMWF - YLVTRHADV - LSAFSLHSY - WMNRLIAFA - YLLPRRGPRL -	0.33	0.55	0.73	0.34	0.56	0.72	0.34	0.56	0.68	0.35
YLVAYQATV - RLIVFPDLGV - TLFGGAYMSK - IPFYGKAI - VLVGGLVLA - CTCGSSDLY - HHHHHH (SEQ ID NO:101)	0.58	0.67	0.41	0.61	0.67	0.44	0.04			

	0.34	0.68	0.44	0.56	0.55	0.33	0.73	0.61	0.9	0.56
YLVTRHADV - WMNRIIFA - CTCGSSDLY - VGIYLLPNR - ILAGYGAGV - LIFCHSKKK - HMWNFISG - IFLLADARV - LIFFLLADA - LSASFHSY -										
GVAGALVAFK - KTSERSQPR - RLGVRAIRK - DLMGYPLV - VLVGGVLAA - LIENILGGWV - YLVAYQATV - YLLPRRGRL - FWAKHMMWF - QLFTFSRR -	0.47	-0.3	-0.07	0.75	0.67	0.94	0.58	0.35	0.72	0.34
LPGCSFSIF - IPFYGKAI - RMYVGGEHR - TLGFCAVMKS - RLIVFPDLGV - VAGALVAFK - HHHHHH (SEQ ID NO:102)	0.82	0.61	0.15	0.41	0.67	0.51	0.04			

HI values (n=3): 1.46 1.68 1.55 1.44 1.61 1.67 2.24 2.07 1.93 0.73 0.10 0.38 1.35 2.36 2.19 1.87 1.65 1.41 1.88 1.77 1.58 1.17 1.23 1.59 1.22

Figure 9

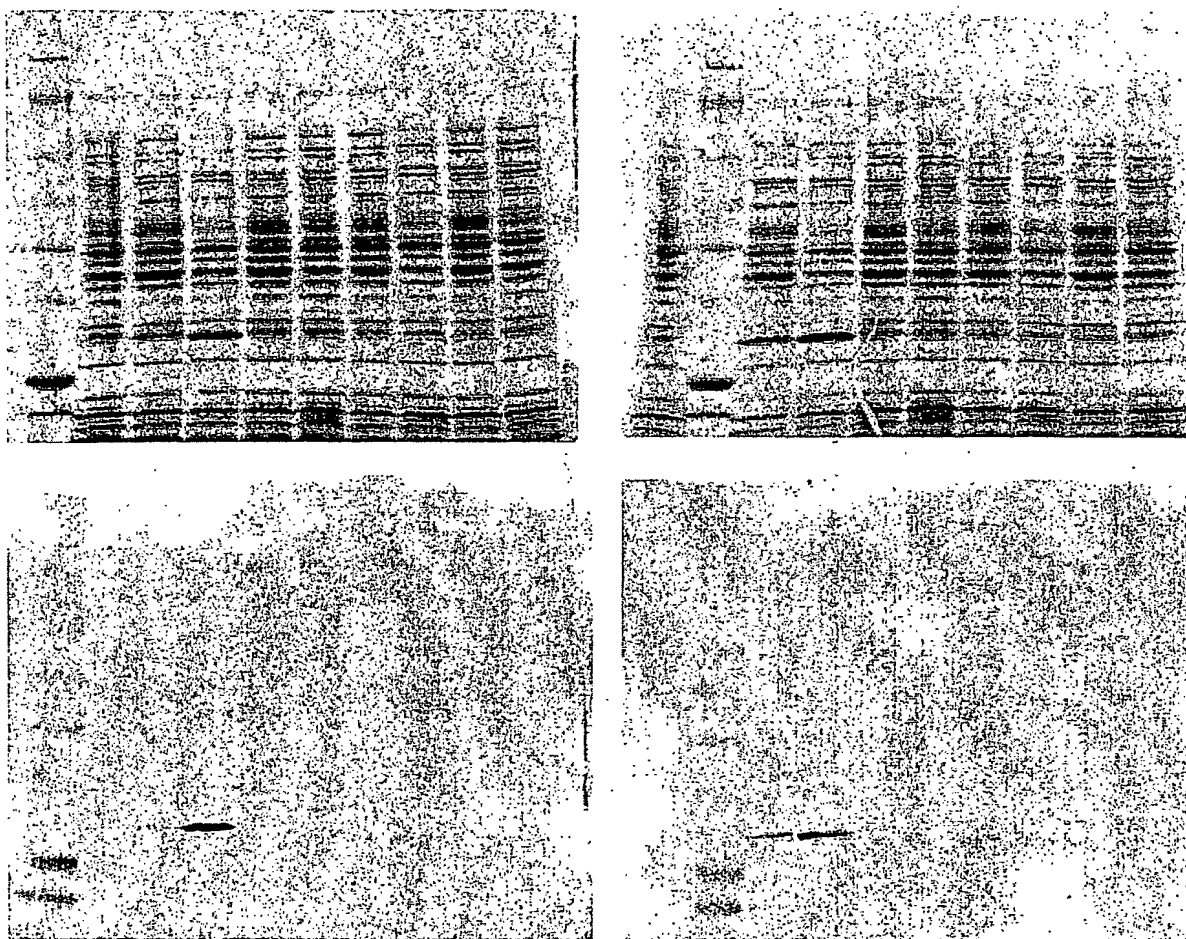
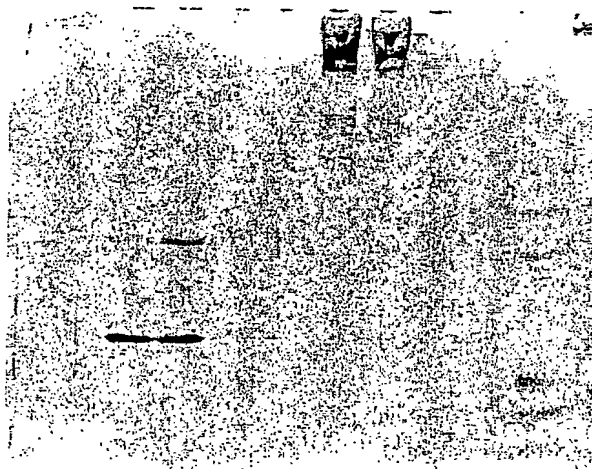
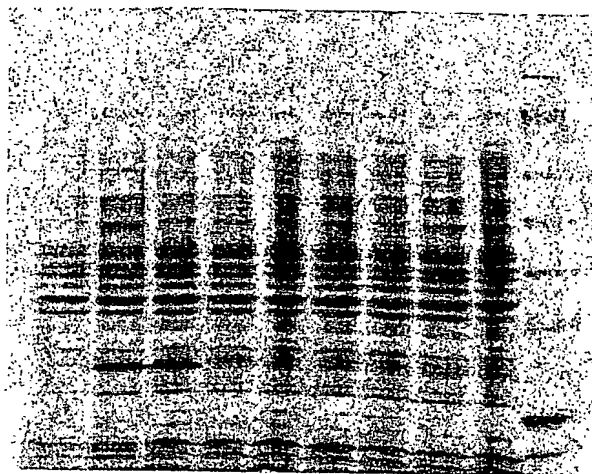
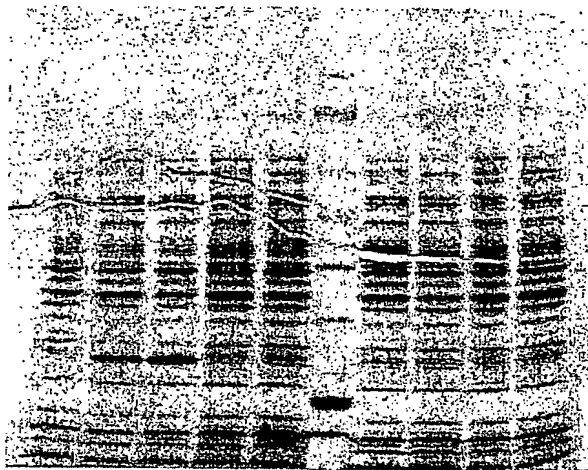


Figure 10



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